<u>IN THE SPECIFICATION</u>:

Please substitute pages 1, 2, 3 and 4 of the International Application with the attached amended pages 1, 2, 3 and 4.

Submitted herewith is a copy of the specification as reformatted and filed in parent Application Serial No. 09/563,048.

**The last paragraph beginning on page 5, line 18, and continuing on to page 6 of the specification is substituted with the following rewritten paragraph.**

Figure 1: Nucleotide sequence of the protein coding (sense) strand of the *X. nematophilus* DNA insert of clone toxb4 (SEQ ID NO: 5). The translation initiation codon (ATG) at nucleotide position 17-19 and the translation termination codon (TAA) at nucleotide position 1121-1123 are indicated by shaded boxes. Locations of oligonucleotide sequences used for sequencing primer design are indicated by arrows and a primer name (TOX F2 (SEQ ID NO: 7), TOX F1 (SEQ ID NO:8), TOX R3 (SEQ ID NO:9) etc., TOX F3 (SEQ ID NO:10), TOX R4 (SEQ ID NO:11), A24AC1 (SEQ ID NO:12)). Arrows directed left-to-right, positioned above the sequence indicate sense-strand primers, arrows directed right-to-left, positioned below the sequence indicate anti-sense primers.


**The first full paragraph on page 6, lines 4-7, of the specification is replaced with the following rewritten paragraph.**

Figure 2: Deduced sequence of the 368 amino acid toxb4 protein from *X. nematophilus* strain A24, derived by conceptual translation of the long open reading frame commencing at nucleotide position 17 and ending at nucleotide position 1120 of the *toxb4* gene sequence (Fig. 1)

(SEQ ID NO: 3).--


**The last full paragraph on page 6, lines 15-21, of the specification is replaced with the following rewritten paragraph.**

Figure 4: Nucleotide sequence of the protein coding (sense) strand of the *P. luminescens* *Hin*d III/*Sma* I DNA fragment (SEQ ID NO:6). Translation initiation (ATG) and termination (TGA) codons are indicated by shaded boxes. Locations of oligonucleotide sequences used for sequencing primer design are indicated by arrows and a primer name as described in the brief description of Fig. 1 (AC4R (SEQ ID NO:13), AC2F (SEQ ID NO:14), AC7R (SEQ ID NO:15), AC6F (SEQ ID NO:16), AC5R (SEQ ID NO:17), AC3F (SEQ ID NO:18), AC8R (SEQ ID NO:19), and V16AC1 (SEQ ID NO:20)). Restriction enzyme sites used for sub-cloning and identification of sequences necessary for toxin activity are underlined and label[l]ed on the figure.


**The last paragraph starting on page 6, line 23, and continuing onto page 7 of the specification is replaced with the following rewritten paragraph.**

Figure 5: Deduced sequence of the 335 amino acid PIV16tox1 protein from *P. luminescens* strain V16/1, derived by conceptual translation of the long open reading frame commencing at nucleotide position 172 and ending at nucleotide position 1179 of the *Hin*d III/*Sma* I restriction enzyme fragment (Fig. 4) (SEQ ID NO:4).--


**The first complete paragraph on page 7, lines 4-8, of the specification is replaced with the following rewritten paragraph.**

Figures 6 A and 6B: Alignment of the nucleotide sequences encompassing the protein open reading frames of the *X. nematophilus* strain A24*toxb4* gene (SEQ ID NO:1) and the *P. luminescens* strain V16/1 *PlV16tox1* gene (SEQ ID NO:2) using the Gap program of the GCG computer software package. The *X. nematophilus* sequence is the upper line and the *P. luminescens* sequence is the lower line.

**The second complete paragraph on page 7, lines 10-14, of the specification is replaced with the following rewritten paragraph.**

Figure 7: Alignment of the deduced protein sequences of the extended open reading frames encoding the *X. nematophilus* A24 toxb4 protein (SEQ ID NO:3) and the *P. luminescens* strain V16/1 PlV16tox1 protein (SEQ ID NO:4) using the Gap program of the GCG computer software package. The *X. nematophilus* sequence is the upper line and the *P. luminescens* sequence is the lower line.

## IN THE DRAWINGS

Figures 6A and 6B are replaced with the attached amended formal drawings of Figures 6A and 6B

## IN THE SEQUENCE LISTING

Please replace pages 34-43 of the specification a copy of the attached substitute Sequence

Listing.